

Appendix III

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with HpaI-MroII (314 bp) deletion fragment of Thudium et al

Alignment of nucleotides 1-314 of SEQ ID NO: 1 of Thudium et al with instant SEQ ID NO: 1

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Score = 614 bits (680), Expect = 2e-180
Identities = 380/401 (94%), Gaps = 8/401 (1%)
Strand=Plus/Plus

Query 782 GTAAGTACCGCCTATAGACTCTATAGCGCCACCCCTTGGCTCTTATGTCATGCTATACT 841
Sbjct 1 GTAAGTACCGCCTATAGACTCTAATAGACACACCCCTTGGCT-CTTATGTCATGCTATACT 59

Query 842 GTTTTGGCTTGGGGCTATACACCCCCCGCTCTCATGTTATAGGTAATGGTATAGCTT 901
Sbjct 60 GTTTTGGCTTGGGGCCTATACACCCCCCGT-CCTTATGCTATAGGTAATGGTATAGCTT 118

Query 902 AGCCTATAGGTGTGGGTATTATGACCATTATGACCACTCCCTATTGGTGACGATCTTT 961
Sbjct 119 AGCCTATAGGTGTGGGTATTATGACCATTATGACCACTCCCTATTGGTGACGATCTTT 178

Query 962 CCATTACTAATCATAACTGGCTCTTTGSCCAACAATCTCTTTATTGGCTATATGCCAAT 1021
Sbjct 179 CCATTACTAATCATAACTGGCTCTTTGSCCAACAATCTCTTATTGGCTATATGCCAAT 238

Query 1022 ACACGTGCTCTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGGTCTCATTTAT 1081
Sbjct 239 ACTCTGCTCTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGGTCT-CATTTAT 297

Query 1082 TATTTACAAAATTCACATATACACACACCCGCTCCGACGTCGCGCAGTTTTATTAAACA 1141
Sbjct 298 TATTTACAAAATTCACATATACACACACCGCTCCGCGCTGCGCGCAGTTTTATTAAACA 357

Query 1142 TAAGCTGGGATCTCC-ACGCGAATCTGGGTAAGTGTTCGG 1181
Sbjct 358 TAGCTGGGATCTCCGAC---ATCTGGGTAAGTGTTCGG 394

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Alignment of nucleotides 710-828 of SEQ ID NO: 1 of Thudium et al with instant SEQ ID NO: 1

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Score = 220 bits (119), Expect = 2e-62
Identities = 119/119 (100%), Gaps = 0/119 (0%)
Strand=Plus/Plus

Query 1183 AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCCGCGCGCCACCAAGACA 1242
Sbjct 710 AACGTTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCCGCGCGGCACCAAGACA 769

Query 1243 TAATAGCTGACAGACTAACAGACTTGTCCTTTTCATGGGGCTTTTTCGACATACCGCTC 1301
Sbjct 770 TAATAGCTGACAGACTAACAGACTTGTCCTTTTCATGGGGCTTTTTCGACATACCGCTC 828

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